

JA

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/509,024
Source: PCF
Date Processed by STIC: 5/26/06

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PCT

RAW SEQUENCE LISTING

DATE: 05/26/2006

PATENT APPLICATION: US/10/509,024

TIME: 07:53:48

Input Set : A:\2005-06-20 2121-0183PUS1.ST25.txt

Output Set: N:\CRF4\05262006\J509024.raw

3 <110> APPLICANT: BOZONET, Sophie Anne Michele et al.

5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR A DEXTRANSACCHARASE

CATALYSING

6 THE SYNTHESIS OF DEXTRAN WITH ALPHA 1,2 OSIDIC SIDECHAINS

8 <130> FILE REFERENCE: 2121-0183PUS1

10 <140> CURRENT APPLICATION NUMBER: US 10/509,024

11 <141> CURRENT FILING DATE: 2004-09-27

13 <150> PRIOR APPLICATION NUMBER: PCT/FR02/00951

14 <151> PRIOR FILING DATE: 2002-03-18

16 <150> PRIOR APPLICATION NUMBER: 0103631

17 <151> PRIOR FILING DATE: 2001-03-16

19 <150> PRIOR APPLICATION NUMBER: 0116495

20 <151> PRIOR FILING DATE: 2001-12-19

22 <160> NUMBER OF SEQ ID NOS: 103

24 <170> SOFTWARE: PatentIn version 3.3

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 855

29 <212> TYPE: PRT

30 <213> ORGANISM: Leuconostoc mesenteroides

32 <220> FEATURE:

33 <223> OTHER INFORMATION: catalytic domain

35 <400> SEQUENCE: 1

36 Asp Met Ser Thr Asn Ala Phe Ser Thr Lys Asn Val Ala Phe Asn His

37 1 5 10 15

39 Asp Ser Ser Ser Phe Asp His Thr Val Asp Gly Phe Leu Thr Ala Asp

40 20 25 30

42 Thr Trp Tyr Arg Pro Lys Ser Ile Leu Ala Asn Gly Thr Thr Trp Arg

43 35 40 45

45 Asp Ser Thr Asp Lys Asp Met Arg Pro Leu Ile Thr Val Trp Trp Pro

46 50 55 60

48 Asn Lys Asn Val Gln Val Asn Tyr Leu Asn Phe Met Lys Ala Asn Gly

49 65 70 75 80

51 Leu Leu Thr Thr Ala Ala Gln Tyr Thr Leu His Ser Asp Gln Tyr Asp

52 85 90 95

54 Leu Asn Gln Ala Ala Gln Asp Val Gln Val Ala Ile Glu Arg Arg Ile

55 100 105 110

57 Ala Ser Glu His Gly Thr Asp Trp Leu Gln Lys Leu Leu Phe Glu Ser

58 115 120 125

60 Gln Asn Asn Asn Pro Ser Phe Val Lys Gln Gln Phe Ile Trp Asn Lys

61 130 135 140

63 Asp Ser Glu Tyr His Gly Gly Gly Asp Ala Trp Phe Gln Gly Gly Tyr

64 145 150 155 160

66 Leu Lys Tyr Gly Asn Asn Pro Leu Thr Pro Thr Thr Asn Ser Asp Tyr

67 165 170 175

p.b

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69 Arg Gln Pro Gly Asn Ala Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
70      180      185      190
72 Asn Ser Asn Pro Val Val Gln Ala Glu Asn Leu Asn Trp Leu His Tyr
73      195      200      205
75 Leu Met Asn Phe Gly Thr Ile Thr Ala Gly Gln Asp Asp Ala Asn Phe
76      210      215      220
78 Asp Ser Ile Arg Ile Asp Ala Val Asp Phe Ile His Asn Asp Thr Ile
79 225      230      235      240
81 Gln Arg Thr Tyr Asp Tyr Leu Arg Asp Ala Tyr Gln Val Gln Gln Ser
82      245      250      255
84 Glu Ala Lys Ala Asn Gln His Ile Ser Leu Val Glu Ala Gly Leu Asp
85      260      265      270
87 Ala Gly Thr Ser Thr Ile His Asn Asp Ala Leu Ile Glu Ser Asn Leu
88      275      280      285
90 Arg Glu Ala Ala Thr Leu Ser Leu Thr Asn Glu Pro Gly Lys Asn Lys
91      290      295      300
93 Pro Leu Thr Asn Met Leu Gln Asp Val Asp Gly Gly Thr Leu Ile Thr
94 305      310      315      320
96 Asp His Thr Gln Asn Ser Thr Glu Asn Gln Ala Thr Pro Asn Tyr Ser
97      325      330      335
99 Ile Ile His Ala His Asp Lys Gly Val Gln Glu Lys Val Gly Ala Ala
100      340      345      350
102 Ile Thr Asp Ala Thr Gly Ala Asp Trp Thr Asn Phe Thr Asp Glu Gln
103      355      360      365
105 Leu Lys Ala Gly Leu Glu Leu Phe Tyr Lys Asp Gln Arg Ala Thr Asn
106      370      375      380
108 Lys Lys Tyr Asn Ser Tyr Asn Ile Pro Ser Ile Tyr Ala Leu Met Leu
109 385      390      395      400
111 Thr Asn Lys Asp Thr Val Pro Arg Met Tyr Tyr Gly Asp Met Tyr Gln
112      405      410      415
114 Asp Asp Gly Gln Tyr Met Ala Asn Lys Ser Ile Tyr Tyr Asp Ala Leu
115      420      425      430
117 Val Ser Leu Met Thr Ala Arg Lys Ser Tyr Val Ser Gly Gly Gln Thr
118      435      440      445
121 Met Ser Val Asp Asn His Gly Leu Leu Lys Ser Val Arg Phe Gly Lys
122      450      455      460
124 Asp Ala Met Thr Ala Asn Asp Leu Gly Thr Ser Ala Thr Arg Thr Glu
125 465      470      475      480
127 Gly Leu Gly Val Ile Ile Gly Asn Asp Pro Lys Leu Gln Leu Asn Asp
128      485      490      495
130 Ser Asp Lys Val Thr Leu Asp Met Gly Ala Ala His Lys Asn Gln Lys
131      500      505      510
133 Tyr Arg Ala Val Ile Leu Thr Thr Arg Asp Gly Leu Ala Thr Phe Asn
134      515      520      525
136 Ser Asp Gln Ala Pro Thr Ala Trp Thr Asn Asp Gln Gly Thr Leu Thr
137      530      535      540
139 Phe Ser Asn Gln Glu Ile Asn Gly Gln Asp Asn Thr Gln Ile Arg Gly
140 545      550      555      560
142 Val Ala Asn Pro Gln Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val

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143          565          570          575
145 Gly Ala Ser Asp Asn Gln Asp Ala Arg Thr Ala Ala Thr Thr Thr Glu
146          580          585          590
148 Asn His Asp Gly Lys Val Leu His Ser Asn Ala Ala Leu Asp Ser Asn
149          595          600          605
151 Leu Ile Tyr Glu Gly Phe Ser Asn Phe Gln Pro Lys Ala Thr Thr His
152          610          615          620
154 Asp Glu Leu Thr Asn Val Val Ile Ala Lys Asn Ala Asp Val Phe Asn
155 625          630          635          640
157 Asn Trp Gly Ile Thr Ser Phe Glu Met Ala Pro Gln Tyr Arg Ser Ser
158          645          650          655
160 Gly Asp His Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe
161          660          665          670
163 Thr Asp Arg Tyr Asp Leu Gly Phe Asn Thr Pro Thr Lys Tyr Gly Thr
164          675          680          685
166 Asp Gly Asp Leu Arg Ala Thr Ile Gln Ala Leu His His Ala Asn Met
167          690          695          700
169 Gln Val Met Ala Asp Val Val Asp Asn Gln Val Tyr Asn Leu Pro Gly
170 705          710          715          720
172 Lys Glu Val Val Ser Ala Thr Arg Ala Gly Val Tyr Gly Asn Asp Asp
173          725          730          735
175 Ala Thr Gly Phe Gly Thr Gln Leu Tyr Val Thr Asn Ser Val Gly Gly
176          740          745          750
178 Gly Gln Tyr Gln Glu Lys Tyr Ala Gly Gln Tyr Leu Glu Ala Leu Lys
179          755          760          765
182 Ala Lys Tyr Pro Asp Leu Phe Glu Gly Lys Ala Tyr Asp Tyr Trp Tyr
183          770          775          780
185 Lys Asn Tyr Ala Asn Asp Gly Ser Asn Pro Tyr Tyr Thr Leu Ser His
186 785          790          795          800
188 Gly Asp Arg Glu Ser Ile Pro Ala Asp Val Ala Ile Lys Gln Trp Ser
189          805          810          815
191 Ala Lys Tyr Met Asn Gly Thr Asn Val Leu Gly Asn Gly Met Gly Tyr
192          820          825          830
194 Val Leu Lys Asp Trp His Asn Gly Gln Tyr Phe Lys Leu Asp Gly Asp
195          835          840          845
197 Lys Ser Thr Leu Pro Gln Ile
198          850          855
201 <210> SEQ ID NO: 2
202 <211> LENGTH: 2835
203 <212> TYPE: PRT
204 <213> ORGANISM: Leuconostoc mesenteroides
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Complete protein DSR-E
209 <400> SEQUENCE: 2
210 Met Arg Asp Met Arg Val Ile Cys Asp Arg Lys Lys Leu Tyr Lys Ser
211 1          5          10          15
213 Gly Lys Val Leu Val Thr Ala Gly Ile Phe Ala Leu Met Met Phe Gly
214          20          25          30
216 Val Thr Thr Ala Ser Val Ser Ala Asn Thr Ile Ala Val Asp Thr Asn

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217          35          40          45
219 His Ser Arg Thr Ser Ala Gln Ile Asn Lys Ser Ala Val Asp Lys Val
220          50          55          60
222 Asn Asp Asp Lys Thr Thr Leu Gly Ala Ala Lys Val Val Ala Val Ala
223 65          70          75          80
225 Thr Thr Pro Ala Thr Pro Val Ala Asp Lys Thr Val Ser Ala Pro Ala
226          85          90          95
228 Ala Asp Lys Ala Val Asp Thr Thr Ser Ser Thr Thr Pro Ala Thr Asp
229          100          105          110
231 Lys Ala Val Asp Thr Thr Pro Thr Thr Pro Ala Ala Asp Lys Ala Val
232          115          120          125
233 Asp Thr Thr Pro Thr Thr Pro Ala Ala Asp Lys Ala Val Asp Thr Thr
234          130          135          140
236 Pro Thr Thr Pro Ala Ala Asn Lys Ala Val Asp Thr Thr Pro Ala Thr
237 145          150          155          160
239 Ala Ala Thr Asp Lys Ala Val Ala Thr Pro Ala Thr Pro Ala Ala Asp
240          165          170          175
242 Lys Leu Ala Asn Thr Thr Pro Ala Thr Asp Lys Ala Val Ala Thr Thr
243          180          185          190
245 Pro Ala Thr Pro Val Ala Asn Lys Ala Ala Asp Thr Ser Ser Ile His
246          195          200          205
248 Asp Gln Pro Leu Asp Thr Asn Val Pro Thr Asp Lys Ser Ala Asn Leu
249          210          215          220
251 Val Ser Thr Thr Gln Lys Ser Thr Asp Asn Gln Gln Val Lys Ser Thr
252 225          230          235          240
254 Glu Thr Ser His Leu Gln Glu Ile Asn Gly Lys Thr Tyr Phe Leu Asp
255          245          250          255
257 Asp Asn Gly Gln Val Lys Lys Asn Phe Thr Ala Ile Ile Asp Gly Lys
258          260          265          270
260 Val Leu Tyr Phe Asp Lys Thr Ser Gly Glu Leu Thr Ala Asn Ala Pro
261          275          280          285
263 Gln Val Thr Lys Gly Leu Val Asn Ile Asp Asn Ala His Asn Ala Ala
264          290          295          300
266 His Asp Leu Thr Ala Asp Asn Phe Thr Asn Val Asp Gly Tyr Leu Thr
267 305          310          315          320
269 Ala Asn Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Thr Thr
270          325          330          335
272 Trp Thr Pro Thr Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ser Trp
273          340          345          350
275 Trp Pro Asp Lys Asn Thr Gln Val Ala Tyr Leu Gln Tyr Met Gln Ser
276          355          360          365
278 Val Gly Met Leu Pro Asp Asp Val Lys Val Ser Asn Asp Asp Asn Met
279          370          375          380
281 Ser Thr Leu Thr Asp Ala Ala Met Thr Val Gln Lys Asn Ile Glu Ser
282 385          390          395          400
284 Arg Ile Gly Val Ser Gly Lys Thr Asp Trp Leu Lys Gln Asp Met Asn
285          405          410          415
287 Lys Leu Ile Asp Ser Gln Ala Asn Trp Asn Ile Asp Ser Glu Ser Lys
288          420          425          430

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290 Gly Asn Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Asp
291          435          440          445
293 Lys Thr Pro Asn Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr Pro
294          450          455          460
296 Thr Asn Gln Thr Gly Gln Ile Thr Asp Pro Ser Lys Gln Gly Gly Tyr
297 465          470          475          480
299 Glu Met Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln
300          485          490          495
303 Ala Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Ile Gly Thr Ile
304          500          505          510
306 Ala Gln Asn Asp Pro Thr Ala Asn Phe Asp Gly Tyr Arg Val Asp Ala
307          515          520          525
309 Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Asp Tyr Phe
310          530          535          540
312 Lys Ala Ala Tyr Gly Thr Gly Lys Thr Glu Ala Asn Ala Asn Asn His
313 545          550          555          560
315 Ile Ser Ile Leu Glu Asp Trp Asp Asn Asn Asp Ser Ala Tyr Ile Lys
316          565          570          575
318 Ala His Gly Asn Asn Gln Leu Thr Met Asp Phe Pro Ala His Leu Ala
319          580          585          590
321 Leu Lys Tyr Ala Leu Asn Met Pro Leu Ala Ala Gln Ser Gly Leu Glu
322          595          600          605
324 Pro Leu Ile Asn Thr Ser Leu Val Lys Arg Gly Lys Asp Ala Thr Glu
325          610          615          620
327 Asn Glu Ala Gln Pro Asn Tyr Ala Phe Ile Arg Ala His Asp Ser Glu
328 625          630          635          640
330 Val Gln Thr Val Ile Ala Gln Ile Ile Lys Asp Lys Ile Asn Thr Lys
331          645          650          655
333 Ser Asp Gly Leu Thr Val Thr Pro Asp Glu Ile Lys Gln Ala Phe Thr
334          660          665          670
336 Ile Tyr Asn Ala Asp Glu Leu Lys Ala Asp Lys Glu Tyr Thr Ala Tyr
337          675          680          685
339 Asn Ile Pro Ala Ser Tyr Ala Val Leu Leu Thr Asn Lys Asp Thr Val
340          690          695          700
342 Pro Arg Val Tyr Tyr Gly Asp Leu Phe Ser Asp Asp Gly Gln Tyr Met
343 705          710          715          720
345 Ser Gln Lys Ser Pro Tyr Tyr Asp Ala Ile Thr Ser Leu Leu Lys Ser
346          725          730          735
348 Arg Ile Lys Tyr Val Ala Gly Gly Gln Ser Met Asn Met Thr Tyr Leu
349          740          745          750
351 His Glu Cys Phe Asp Pro Ala Lys Asn Glu Thr Lys Pro Gln Gly Val
352          755          760          765
354 Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala Asp Asp Leu
355          770          775          780
357 Gly Asn Ser Asp Thr Arg Gln Gln Gly Ile Gly Leu Val Ile Asn Asn
358 785          790          795          800
360 Lys Pro Phe Leu Asn Leu Asn Asp Asp Glu Gln Ile Val Leu Asn Met
361          805          810          815
364 Gly Ala Ala His Lys Asn Gln Ala Tyr Arg Pro Leu Met Leu Thr Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/509,024

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Input Set : A:\2005-06-20 2121-0183PUS1.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:39; Xaa Pos. 6,28

Seq#:43; Xaa Pos. 4,6,9,10,11

Seq#:61; Xaa Pos. 12

VERIFICATION SUMMARY

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L:1538 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0

M:341 Repeated in SeqNo=39

L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0

L:1855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0